SEQUENCE LISTING

(1)   GENERAL INFORMATION:

    (i)   APPLICANT:
        (A) NAME: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
                  REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH
                  AND HUMAN SERVICES
        (B) STREET: BOX OTT
        (C) CITY: BETHESDA
        (D) STATE OR PROVINCE: MARYLAND
        (E) COUNTRY: UNITED STATES OF AMERICA
        (F) POSTAL CODE: 20892

    (i)   APPLICANT:
        (A) NAME: PAVLAKIS, GEORGE N.
        (B) STREET: 9 PURDUE COURT
        (C) CITY: ROCKVILLE
        (D) STATE OR PROVINCE: MARYLAND
        (E) COUNTRY: UNITED STATES OF AMERICA
        (F) POSTAL CODE: 20850

    (i)   APPLICANT:
        (A) NAME: FELBER, BARBARA K.
        (B) STREET: 9 PURDUE COURT
        (C) CITY: ROCKVILLE
        (D) STATE OR PROVINCE: MARYLAND
        (E) COUNTRY: UNITED STATES OF AMERICA
        (F) POSTAL CODE: 20850

    (ii) TITLE OF INVENTION: METHOD OF ELIMINATING
        INHIBITORY/INSTABILITY REGIONS OF mRNA

    (iii) NUMBER OF SEQUENCES: 130

    (iv) CORRESPONDENCE ADDRESS:
        (A)   ADDRESSEE: MORGAN & FINNEGAN
        (B)   STREET: 345 PARK AVENUE
        (C)   CITY: NEW YORK
        (D)   STATE: NEW YORK
        (E)   COUNTRY: USA
        (F)   ZIP: 10154

    (v)   COMPUTER READABLE FORM:
        (A)   MEDIUM TYPE: FLOPPY DISK
        (B)   COMPUTER: IBM PC COMPATIBLE
        (C)   OPERATING SYSTEM: PC-DOS/MS-DOS
        (D)   SOFTWARE: WORDPERFECT 5.1

    (vi) CURRENT APPLICATION DATA:
        (A)   APPLICATION NUMBER: TO BE ASSIGNED
        (B)   FILING DATE: 02-MAY-1997
        (C)   CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A)   APPLICATION NUMBER: US 08/050,478
        (B)   FILING DATE: 26-OCT-1994
        (C)   CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A)   APPLICATION NUMBER: PCT/US93/02908
        (B)   FILING DATE: 29-MAR-1993
        (C)   CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A)   APPLICATION NUMBER: US 07/858,747
        (B)   FILING DATE: 27-MAR-1992
        (C)   CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A)   NAME: MORRY, MARY J.

```
            (B)  REGISTRATION NUMBER:  34,398
            (C)  REFERENCE/DOCKET NUMBER:  2026-4006US1

      (ix)  TELECOMMUNICATION INFORMATION:
            (A)  TELEPHONE:  (212)758-4800
            (B)  TELEFAX:  (212)751-6849

(2)     INFORMATION FOR SEQ ID NO: 1:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  396 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTIONS:SEQ ID NO: 1:
```

ATGGGTGCGA GAGCGTCAGT ATTAAGCGGG GGAGAATTAG ATCGATGGGA AAAAATTCGG   60

TTAAGGCCAG GGGGAAAGAA AAAATATAAA TTAAAACATA TAGTATGGGC AAGCAGGGAG   120

CTAGAACGAT TCGCAGTTAA TCCTGGCCTG TTAGAAACAT CAGAAGGCTG TAGACAAATA   180

CTGGGACAGC TACAACCATC CCTTCAGACA GGATCAGAAG AACTTAGATC ATTATATAAT   240

ACAGTAGCAA CCCTCTATTG TGTGCATCAA AGGATAGAGA TAAAAGACAC CAAGGAAGCT   300

TTAGACAAGA TAGAGGAAGA GCAAAACAAA AGTAAGAAAA AAGCACAGCA AGCAGCAGCT   360

GACACAGGAC ACAGCAATCA GGTCAGCCAA AATTAC   396


```
(3)  INFORMATION FOR SEQ ID NO: 2:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  51 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTIONS:SEQ ID NO: 2:
```

CCAGGGGGAA AGAAAAAATA TAAATTAAAA CATATAGTAT GGGCAAGCAG G   51


```
(4)  INFORMATION FOR SEQ ID NO: 3:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  48 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTIONS:SEQ ID NO: 3:
```

CCTTCAGACA GGATCAGAAG AACTTAGATC ATTATATAAT ACAGTAGC   48


```
(5)     INFORMATION FOR SEQ ID NO: 4:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  50 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTIONS:SEQ ID NO: 4:
```

ACCCTCTATT GTGTGCATCA AAGGATAGAG ATAAAAGACA CCAAGGAAGC   50

(6) INFORMATION FOR SEQ ID NO: 5:
    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 50 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTIONS:SEQ ID NO: 5:

GAGCAAAACA AAAGTAAGAA AAAAGCACAG CAAGCAGCAG CTGACACAGG   50

(7) INFORMATION FOR SEQ ID NO: 6:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 51 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CCAGGGGGAA AGAAGAAGTA CAAGCTAAAG CACATCGTAT GGGCAAGCAG G   51

(8) INFORMATION FOR SEQ ID NO: 7:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 48 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCTTCAGACA GGATCAGAGG AGCTTCGATC ACTATACAAC ACAGTAGC   48

(9) INFORMATION FOR SEQ ID NO: 8:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 50 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ACCCTCTATT GTGTGCACCA GCGGATCGAG ATCAAGGACA CCAAGGAAGC   50

(10) INFORMATION FOR SEQ ID NO: 9:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 50 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAGCAAAACA AGTCCAAGAA GAAGGCCCAG CAGGCAGCAG CTGACACAGG   50

(11) INFORMATION FOR SEQ ID NO: 10:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 68 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAATAGTGCT GTTAACCTCC TGAACGCTAC CGCTATCGCC GTGGCGGAAG GAACCGACAG   60

GGTTATAG   68

(12) INFORMATION FOR SEQ ID NO: 11:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 62 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AAGTATTACA AGCCGCCTAC CGCGCCATCA GACATATCCC CCGCCGCATC CGCCAGGGCT   60

TG   62

(13) INFORMATION FOR SEQ ID NO: 12:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCTATAAGAT GGGCGGTAAA TGGAGCAAGT CCTCCGTCAT CGGCTGGCCT GCTGTAAG   58

(14) INFORMATION FOR SEQ ID NO: 13:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGAAAGAATG CGCAGGGCCG AACCCGCCGC CGACGGAGTT GGCGCCGTAT CTCGAGAC   58

(15) INFORMATION FOR SEQ ID NO: 14:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 62 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTAGAAAAAC ACGGCGCCAT TACCTCCTCT AACACCGCCG CCAATAACGC CGCTTGTGCC   60

TG   62

(16) INFORMATION FOR SEQ ID NO: 15:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCTAGAAGCA CAGGAAGAAG AGGAAGTCGG CTTCCCCGTT ACCCCTCAGG TACCTTTAAG   60

(17) INFORMATION FOR SEQ ID NO: 16:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 43 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TGAAAACGTT CGCATGTGTC GCTACGTTGC TTACTAAGAT GGA   43

(18) INFORMATION FOR SEQ ID NO: 17:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 43 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCTCAGATA CCTAGCTTCA TATTGCCTTA TTGTCTACCT TGA   43

(19) INFORMATION FOR SEQ ID NO: 18:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCCTGTGAG TAGGCACTGA AGGACAGCCA TACGTAACAT ACAAGTGCCA   50

(20) INFORMATION FOR SEQ ID NO: 19:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 51 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AGCAGCAGCA ATGAACCTAG TAGCGATAGC CTGAGTAGCC CTACGCTGCT G   51

(21) INFORMATION FOR SEQ ID NO: 20:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ACCCCGAGGC AGATAGCTTT CCATCCTGCG CTGCCGCTCA CCGCAAGGGC   50

(22) INFORMATION FOR SEQ ID NO: 21:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 61 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTGCACAGTG GAAGCCTCGG AATGGGCCCT ATGGCTACCG AATTGGAACC ACTGTGCACT C   61

(23) INFORMATION FOR SEQ ID NO: 22:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 47 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CACCTAGAAC TTTAAATGCA TGGGTAAAAG TAGTAGAAGA GAAGGCT   47

(24) INFORMATION FOR SEQ ID NO: 23:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 47 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CACCTAGAAC CCTGAACGCC TGGGTGAAGG TGGTAGAAGA GAAGGCT   47

(25) INFORMATION FOR SEQ ID NO: 24:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 45 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCACCCCACA AGATTTAAAC ACCATGCTAA ACACAGTGGG GGGAC   45

(26) INFORMATION FOR SEQ ID NO: 25:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 45 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCACCCCACA GGACCTGAAC ACGATGTTGA ACACCGTGGG GGGAC   45

(27) INFORMATION FOR SEQ ID NO: 26:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 35 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE

```
            (D)  TOPOLOGY:  LINEAR

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 26:

     CAGTAGGAGA AATTTATAAA AGATGGATAA TCCTG                                    35


        (28) INFORMATION FOR SEQ ID NO: 27:

            (i)   SEQUENCE CHARACTERISTICS:
                  (A)  LENGTH:  35 BASE PAIRS
                  (B)  TYPE:  NUCLEIC ACID
                  (C)  STRANDEDNESS:  SINGLE
                  (D)  TOPOLOGY:  LINEAR

            (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 27:

     CAGTAGGAGA GATCTACAAG AGGTGGATAA TCCTG                                    35


        (29) INFORMATION FOR SEQ ID NO: 28:

            (i)   SEQUENCE CHARACTERISTICS:
                  (A)  LENGTH:  36 BASE PAIRS
                  (B)  TYPE:  NUCLEIC ACID
                  (C)  STRANDEDNESS:  SINGLE
                  (D)  TOPOLOGY:  LINEAR

            (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 28:

     GGATTAAATA AAATAGTAAG AATGTATAGC CCTACC                                   36


        (30) INFORMATION FOR SEQ ID NO: 29:

            (i)   SEQUENCE CHARACTERISTICS:
                  (A) .LENGTH:  36 BASE PAIRS
                  (B)  TYPE:  NUCLEIC ACID
                  (C)  STRANDEDNESS:  SINGLE
                  (D)  TOPOLOGY:  LINEAR

            (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 29:

     GGATTGAACA AGATCGTGAG GATGTATAGC CCTACC                                   36


        (31) INFORMATION FOR SEQ ID NO: 30:

            (i)   SEQUENCE CHARACTERISTICS:
                  (A)  LENGTH:  41 BASE PAIRS
                  (B)  TYPE:  NUCLEIC ACID
                  (C)  STRANDEDNESS:  SINGLE
                  (D)  TOPOLOGY:  LINEAR

            (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 30:

     ACCGGTTCTA TAAAACTCTA AGAGCCGAGC AAGCTTCACA G                             41


        (32) INFORMATION FOR SEQ ID NO: 31:

            (i)   SEQUENCE CHARACTERISTICS:
                  (A)  LENGTH:  41 BASE PAIRS
                  (B)  TYPE:  NUCLEIC ACID
                  (C)  STRANDEDNESS:  SINGLE
                  (D)  TOPOLOGY:  LINEAR

            (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 31:

     ACCGGTTCTA CAAGACCCTG CGGGCTGAGC AAGCTTCACA G                             41
```

(33) INFORMATION FOR SEQ ID NO: 32:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 44 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ATTGTAAGAC TATTTTAAAA GCATTGGGAC CAGCGGCTAC ACTA   44

(34) INFORMATION FOR SEQ ID NO: 33:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 44 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATTGTAAGAC CATCCTGAAG GCTCTCGGCC CAGCGGCTAC ACTA   44

(35) INFORMATION FOR SEQ ID NO: 34:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 51 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGAGTTTTGG CTGAAGCAAT GAGCCAAGTA ACAAATTCAG CTACCATAAT G   51

(36) INFORMATION FOR SEQ ID NO: 35:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 51 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AGAGTTTTGG CCGAGGCGAT GAGCCAGGTG ACGAACTCGG CGACCATAAT G   51

(37) INFORMATION FOR SEQ ID NO: 36:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 51 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CAGAGAGGCA ATTTTAGGAA CCAAAGAAAG ATTGTTAAGT GTTTCAATTG T   51

(38) INFORMATION FOR SEQ ID NO: 37:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 51 BASE PAIRS
        (B) TYPE: NUCLEIC ACID

294280_1

```
          (C)  STRANDEDNESS:  SINGLE
          (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 37:
```

CAGAGAGGCA ACTTCCGGAA CCAGCGGAAG ATCGTCAAGT GTTTCAATTG T   51

(39) INFORMATION FOR SEQ ID NO: 38:

```
     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH:  48 BASE PAIRS
          (B)  TYPE:  NUCLEIC ACID
          (C)  STRANDEDNESS:  SINGLE
          (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 38:
```

GAAGGGCACA CAGCCAGAAA TTGCAGGGCC CCTAGGAAAA AGGGCTGT   48

(40) INFORMATION FOR SEQ ID NO: 39:

```
     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH:  48 BASE PAIRS
          (B)  TYPE:  NUCLEIC ACID
          (C)  STRANDEDNESS:  SINGLE
          (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 39:
```

GAAGGGCACA CCGCCAGGAA CTGCCGGGCC CCCCGGAAGA AGGGCTGT   48

(41) INFORMATION FOR SEQ ID NO: 40:

```
     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH:  51 BASE PAIRS
          (B)  TYPE:  NUCLEIC ACID
          (C)  STRANDEDNESS:  SINGLE
          (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 40:
```

TGTGGAAAGG AAGGACACCA AATGAAAGAT TGTACTGAGA GACAGGCTAA T   51

(42) INFORMATION FOR SEQ ID NO: 41:

```
     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH:  51 BASE PAIRS
          (B)  TYPE:  NUCLEIC ACID
          (C)  STRANDEDNESS:  SINGLE
          (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 41:
```

TGTGGAAAGG AGGGGCACCA GATGAAGGAC TGCACGGAGC GGCAGGCTAA T   51

(43) INFORMATION FOR SEQ ID NO: 42:

```
     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH:  58 BASE PAIRS
          (B)  TYPE:  NUCLEIC ACID
          (C)  STRANDEDNESS:  SINGLE
          (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 42:
```

CCCCTCGTCA CAATAAAGAT AGGGGGGCAA CTAAAGGAAG CTCTATTAGA TACAGGAG   58

(44) INFORMATION FOR SEQ ID NO: 43:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 58 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCCCTCGTCA CAGTAAGGAT CGGGGGGCAA CTCAAGGAAG CGCTGCTCGA TACAGGAG   58

(45) INFORMATION FOR SEQ ID NO: 44:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 52 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GATAGGGGGA ATTGGAGGTT TTATCAAAGT AAGACAGTAT GATCAGATAC TC   52

(46) INFORMATION FOR SEQ ID NO: 45:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 52 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GATAGGGGGG ATCGGGGGCT TCATCAAGGT GAGGCAGTAC GACCAGATAC TC   52

(47) INFORMATION FOR SEQ ID NO: 46:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 48 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

CCTATTGAGA CTGTACCAGT AAAATTAAAG CCAGGAATGG ATGGCCCA   48

(48) INFORMATION FOR SEQ ID NO: 47:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 48 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTATTGAGA CGGTGCCCGT GAAGTTGAAG CCGGGGATGG ATGGCCCA   48

(49) INFORMATION FOR SEQ ID NO: 48:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 55 BASE PAIRS

```
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 48:
```

CAATGGCCAT TGACAGAAGA AAAAATAAAA GCATTAGTAG AAATTTGTAC AGAGA   55

```
   (50) INFORMATION FOR SEQ ID NO: 49:

     (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  55 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 49:
```

CAATGGCCAT TGACGGAAGA GAAGATCAAG GCCTTAGTCG AAATCTGTAC AGAGA   55

```
   (51) INFORMATION FOR SEQ ID NO: 50:

     (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  51 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 50:
```

TTCAGGAAGT ATACTGCATT TACCATACCT AGTATAAACA ATGAGACACC A   51

```
   (52) INFORMATION FOR SEQ ID NO: 51:

     (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  51 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 51:
```

TTCAGGAAGT ACACGGCGTT CACCATCCCG AGCATCAACA ACGAGACACC A   51

```
   (53) INFORMATION FOR SEQ ID NO: 52:

     (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  49 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 52:
```

TTAGTGGGGA AATTGAATTG GGCAAGTCAG ATTTACCCAG GGATTAAAG   49

```
   (54) INFORMATION FOR SEQ ID NO: 53:

     (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  49 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

     (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 53:
```

TTAGTGGGGA AGGTGAACTG GGCGAGCCAG ATCTACCCGG GGATTAAAG   49

(55) INFORMATION FOR SEQ ID NO: 54:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 53 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GGCCAATGGA CATATCAAAT TTATCAAGAG CCATTTAAAA ATCTGAAAAC AGG   53

(56) INFORMATION FOR SEQ ID NO: 55:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 53 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GGCCAATGGA CGTACCAGAT CTACCAGGAG CCGTTCAAGA ACCTGAAAAC AGG   53

(57) INFORMATION FOR SEQ ID NO: 56:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 49 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGGGGAAAGA CTCCTAAATT TAAACTGCCC ATACAAAAGG AAACATGGG   49

(58) INFORMATION FOR SEQ ID NO: 57:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 49 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGGGGAAAGA CGCCGAAGTT CAAGCTGCCC ATCCAGAAGG AGACATGGG   49

(59) INFORMATION FOR SEQ ID NO: 58:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 50 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GAAGACTGAG TTACAAGCAA TTTATCTAGC TTTGCAGGAT TCGGGATTAG   50

(60) INFORMATION FOR SEQ ID NO: 59:

        (i)   SEQUENCE CHARACTERISTICS:

```
            (A)  LENGTH:  50 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 59:
```

GAAGACTGAG CTGCAGGCGA TCTACCTGGC GCTGCAGGAC TCGGGATTAG   50

```
   (61) INFORMATION FOR SEQ ID NO: 60:

      (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  56 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 60:
```

GTTAGTCAAT CAAATAATAG AGCAGTTAAT AAAAAAGGAA AAGGTCTATC TGGCAT   56

```
   (62) INFORMATION FOR SEQ ID NO: 61:

      (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  56 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 61:
```

GTTAGTCAAC CAAATCATCG AGCAGCTGAT CAAGAAGGAG AAGGTGTATC TGGCAT   56

```
   (63) INFORMATION FOR SEQ ID NO: 62:

      (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  52 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 62:
```

GTCAGTGCTG GAATCAGGAA AGTACTATTT TTAGATGGAA TAGATAAGGC CC   52

```
   (64) INFORMATION FOR SEQ ID NO: 63:

      (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  52 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 63:
```

GTCAGTGCTG GGATCCGGAA GGTGCTATTC CTGGACGGGA TCGATAAGGC CC   52

```
   (65) INFORMATION FOR SEQ ID NO: 64:

      (i)   SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  58 BASE PAIRS
            (B)  TYPE:  NUCLEIC ACID
            (C)  STRANDEDNESS:  SINGLE
            (D)  TOPOLOGY:  LINEAR

      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 64:
```

GAACATGAGA AATATCACAG TAATTGGAGA GCAATGGCTA GTGATTTTAA CCTGCCAC   58

(66) INFORMATION FOR SEQ ID NO: 65:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 58 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAACATGAGA AGTACCACTC CAACTGGCGC GCTATGGCCA GCGACTTCAA CCTGCCAC   58

(67) INFORMATION FOR SEQ ID NO: 66:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 52 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GGAATATGGC AACTAGATTG TACACATTTA GAAGGAAAAG TTATCCTGGT AG   52

(68) INFORMATION FOR SEQ ID NO: 67:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 52 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GGAATATGGC AGCTGGACTG CACGCACCTG GAGGGGAAGG TGATCCTGGT AG   52

(69) INFORMATION FOR SEQ ID NO: 68:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 66 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GCAGAAGTTA TTCCAGCAGA AACAGGGCAG GAAACAGCAT ATTTTCTTTT AAAATTAGCA   60

GGAAGA   66

(70) INFORMATION FOR SEQ ID NO: 69:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 66 BASE PAIRS
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: SINGLE
              (D) TOPOLOGY: LINEAR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GCAGAAGTTA TCCCTGCTGA AACTCGGCAG GAGACCGCCT ACTTCCTGCT CAAACTCGCA   60

GGAAGA   66

(71) INFORMATION FOR SEQ ID NO: 70:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 55 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TGGCCAGTAA AAACAATACA TACTGACAAT GGCAGCAATT TCACCGGTGC TACGG   55

(72) INFORMATION FOR SEQ ID NO: 71:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 55 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TGGCCAGTGA AGACGATCCA CACGGACAAC GGAAGCAACT TCACTGGTGC TACGG   55

(73) INFORMATION FOR SEQ ID NO: 72:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 52 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GGAGTAGTAG AATCTATGAA TAAAGAATTA AAGAAAATTA TAGGACAGGT AA   52

(74) INFORMATION FOR SEQ ID NO: 73:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 52 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GGAGTAGTAG AATCCATGAA CAAGGAACTG AAGAAGATCA TCGGACAGGT AA   52

(75) INFORMATION FOR SEQ ID NO: 74:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 55 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TGGCCAGTAA AAACAATACA CACGGACAAC GGAAGCAACT TCACTGGTGC TACGG   55

(76) INFORMATION FOR SEQ ID NO: 75:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 45 BASE PAIRS

```
        (B)  TYPE:  NUCLEIC ACID
        (C)  STRANDEDNESS:  SINGLE
        (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 75:
```

CTTGGGATGT TGATGATCTG TAGTGCTACA GAAAAATTGT GGGTC   45

(77) INFORMATION FOR SEQ ID NO: 76:

```
    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH:  45 BASE PAIRS
        (B)  TYPE:  NUCLEIC ACID
        (C)  STRANDEDNESS:  SINGLE
        (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 76:
```

CTTGGGATGC TGATGATCTG CAGCGCCACC GAGAAGCTGT GGGTC   45

(78) INFORMATION FOR SEQ ID NO: 77:

```
    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH:  23 BASE PAIRS
        (B)  TYPE:  NUCLEIC ACID
        (C)  STRANDEDNESS:  SINGLE
        (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 77:
```

ATTATGGGGT ACCTGTGTGG AAG   23

(79) INFORMATION FOR SEQ ID NO: 78:

```
    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH:  23 BASE PAIRS
        (B)  TYPE:  NUCLEIC ACID
        (C)  STRANDEDNESS:  SINGLE
        (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 78:
```

ATTATGGCGT GCCCGTGTGG AAG   23

(80) INFORMATION FOR SEQ ID NO: 79:

```
    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH:  37 BASE PAIRS
        (B)  TYPE:  NUCLEIC ACID
        (C)  STRANDEDNESS:  SINGLE
        (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 79:
```

CACTCTATTT TGTGCATCAG ATGCTAAAGC ATATGAT   37

(81) INFORMATION FOR SEQ ID NO: 80:

```
    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH:  37 BASE PAIRS
        (B)  TYPE:  NUCLEIC ACID
        (C)  STRANDEDNESS:  SINGLE
        (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 80:
```

CACTCTATTC TGCGCCTCCG ACGCCAAGGC ATATGAT   37

(82) INFORMATION FOR SEQ ID NO: 81:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACAGAGGTAC ATAATGTTTG GGCCAC   26

(83) INFORMATION FOR SEQ ID NO: 82:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ACAGAGGTGC ACAACGTCTG GGCCAC   26

(84) INFORMATION FOR SEQ ID NO: 83:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 52 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CCAACCCACA AGAAGTAGTA TTGGTAAATG TGACAGAAAA TTTTAACATG TG   52

(85) INFORMATION FOR SEQ ID NO: 84:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 52 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CCAACCCCCA GGAGGTGGTG CTGGTGAACG TGACCGAGAA CTTCAACATG TG   52

(86) INFORMATION FOR SEQ ID NO: 85:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TAACCCCACT CTGTGTTAGT TTAAAGTGCA CTGATTTGAA GAATG   45

(87) INFORMATION FOR SEQ ID NO: 86:

    (i)   SEQUENCE CHARACTERISTICS:

2042800_1

                    (A) LENGTH: 45 BASE PAIRS
                    (B) TYPE: NUCLEIC ACID
                    (C) STRANDEDNESS: SINGLE
                    (D) TOPOLOGY: LINEAR

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

TAACCCCCCT CTGCGTGAGC CTGAAGTGCA CCGACCTGAA GAATG   45

    (88) INFORMATION FOR SEQ ID NO: 87:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 30 BASE PAIRS
                    (B) TYPE: NUCLEIC ACID
                    (C) STRANDEDNESS: SINGLE
                    (D) TOPOLOGY: LINEAR

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

ATCAGCACAA GCATAAGAGG TAAGGTGCAG   30

    (89) INFORMATION FOR SEQ ID NO: 88:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 30 BASE PAIRS
                    (B) TYPE: NUCLEIC ACID
                    (C) STRANDEDNESS: SINGLE
                    (D) TOPOLOGY: LINEAR

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

ATCAGCACCA GCATCCGCGG CAAGGTGCAG   30

    (90) INFORMATION FOR SEQ ID NO: 89:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 33 BASE PAIRS
                    (B) TYPE: NUCLEIC ACID
                    (C) STRANDEDNESS: SINGLE
                    (D) TOPOLOGY: LINEAR

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GAATATGCAT TTTTTTATAA ACTTGATATA ATA   33

    (91) INFORMATION FOR SEQ ID NO: 90:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 33 BASE PAIRS
                    (B) TYPE: NUCLEIC ACID
                    (C) STRANDEDNESS: SINGLE
                    (D) TOPOLOGY: LINEAR

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GAATATGCCT TCTTCTACAA GCTGGATATA ATA   33

    (92) INFORMATION FOR SEQ ID NO: 91:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 27 BASE PAIRS
                    (B) TYPE: NUCLEIC ACID
                    (C) STRANDEDNESS: SINGLE
                    (D) TOPOLOGY: LINEAR

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CCAATAGATA ATGATACTAC CAGCTAT 27

(93) INFORMATION FOR SEQ ID NO: 92:

    (i)   SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 27 BASE PAIRS
           (B) TYPE: NUCLEIC ACID
           (C) STRANDEDNESS: SINGLE
           (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCAATAGCTA AGGACACCAC CAGCTAT 27

(94) INFORMATION FOR SEQ ID NO: 93:

    (i)   SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 45 BASE PAIRS
           (B) TYPE: NUCLEIC ACID
           (C) STRANDEDNESS: SINGLE
           (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GCCCCGGCTG GTTTTGCGAT TCTAAAATGT AATAATAAGA CGTTC 45

(95) INFORMATION FOR SEQ ID NO: 94:

    (i)   SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 45 BASE PAIRS
           (B) TYPE: NUCLEIC ACID
           (C) STRANDEDNESS: SINGLE
           (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GCCCCGGCCG GCTTCGCGAT CCTGAAGTGC AACAACAAGA CGTTC 45

(96) INFORMATION FOR SEQ ID NO: 95:

    (i)   SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 42 BASE PAIRS
           (B) TYPE: NUCLEIC ACID
           (C) STRANDEDNESS: SINGLE
           (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CAACTGCTGT TAAATGGCAG TCTAGCAGAA GAAGAGGTAG TA 42

(97) INFORMATION FOR SEQ ID NO: 96:

    (i)   SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 42 BASE PAIRS
           (B) TYPE: NUCLEIC ACID
           (C) STRANDEDNESS: SINGLE
           (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CAACTGCTGC TGAACGGCAG CCTGGCCGAG GAGGAGGTAG TA 42

(98) INFORMATION FOR SEQ ID NO: 97:

        (i)   SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 35 BASE PAIRS
               (B) TYPE: NUCLEIC ACID
               (C) STRANDEDNESS: SINGLE
               (D) TOPOLOGY: LINEAR

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TCTGTCAATT TCACGGACAA TGCTAAAACC ATAAT   35

(99) INFORMATION FOR SEQ ID NO: 98:

        (i)   SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 35 BASE PAIRS
               (B) TYPE: NUCLEIC ACID
               (C) STRANDEDNESS: SINGLE
               (D) TOPOLOGY: LINEAR

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TCTGCCAACT TCACCGACAA CGCCAAGACC ATAAT   35

(100) INFORMATION FOR SEQ ID NO: 99:

        (i)   SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 32 BASE PAIRS
               (B) TYPE: NUCLEIC ACID
               (C) STRANDEDNESS: SINGLE
               (D) TOPOLOGY: LINEAR

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CTGAACACAT CTGTAGAAAT TAATTGTACA AG   32

(101) INFORMATION FOR SEQ ID NO: 100:

        (i)   SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 32 BASE PAIRS
               (B) TYPE: NUCLEIC ACID
               (C) STRANDEDNESS: SINGLE
               (D) TOPOLOGY: LINEAR

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CTGAACCAGT CCGTGGAGAT CAACTGTACA AG   32

(102) INFORMATION FOR SEQ ID NO: 101:

        (i)   SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 31 BASE PAIRS
               (B) TYPE: NUCLEIC ACID
               (C) STRANDEDNESS: SINGLE
               (D) TOPOLOGY: LINEAR

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CAACAACAAT ACAAGAAAAA GAATCCGTAT C   31

(103) INFORMATION FOR SEQ ID NO: 102:

        (i)   SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 31 BASE PAIRS
               (B) TYPE: NUCLEIC ACID
               (C) STRANDEDNESS: SINGLE
               (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CAACAACAAC ACCGGCAAGC GCATCCGTAT C   31

(104) INFORMATION FOR SEQ ID NO: 103:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 47 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

GCTAGCAAAT TAAGAGAACA ATTTGGAAAT AATAAAACAA TAATCTT   47

(105) INFORMATION FOR SEQ ID NO: 104:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 47 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GCTAGCAAGC TGCGCGAGCA GTACGGGAAC AACAAGACCA TAATCTT   47

(106) INFORMATION FOR SEQ ID NO: 105:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

TTCTACTGTA ATTCAACACA ACTGTTTAAT AGTACTTGGT TTAAT   45

(107) INFORMATION FOR SEQ ID NO: 106:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TTCTACTGGA ACTCCACCCA GCTGTTCAAC AGCACCTGGT TTAAT   45

(108) INFORMATION FOR SEQ ID NO: 107:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 43 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CACAATCACC CTCCCATGCA GAATAAAACA AATTATAAAC ATG   43

(109) INFORMATION FOR SEQ ID NO: 108:

(i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 43 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CACAATCACC CTGCCCTGCC GCATCAAGCA GATCATAAAC ATG   43

(110) INFORMATION FOR SEQ ID NO: 109:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCAGTGGA CAAATTAGAT GTTCATCAAA TATTACAGGG CTGCTA   46

(111) INFORMATION FOR SEQ ID NO: 110:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

CATCAGCGGC CAGATCCGCT GCTCCTCCAA CATCACCGGG CTGCTA   46

(112) INFORMATION FOR SEQ ID NO: 111:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GAGGGACAAT TGGAGAAGTG AATTATATAA ATATAAAGTA GTAAAAATTG AACCATTA   58

(113) INFORMATION FOR SEQ ID NO: 112:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GAGGGACAAC TGGAGGAGCG AGCTGTACAA GTACAAGGTG GTGAAGATCG AACCATTA   58

(114) INFORMATION FOR SEQ ID NO: 113:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 40 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

GCCTTGGAAT GCTAGTTGGA GTAATAAATC TCTGGAACAG   40

(115) INFORMATION FOR SEQ ID NO: 114:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 40 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

GCCTTGGAAC GCCAGCTGGA GCAACAAGTC CCTGGAACAG   40

(116) INFORMATION FOR SEQ ID NO: 115:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GAGTGGGACA GAGAAATTAA CAATTACACA AG   32

(117) INFORMATION FOR SEQ ID NO: 116:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GAGTGGGACC GCGAGATCAA CAACTACACA AG   32

(118) INFORMATION FOR SEQ ID NO: 117:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACACTCCT TAATTGAAGA ATCGCAAAAC CAGCAAGAAA AGAATGAA   48

(119) INFORMATION FOR SEQ ID NO: 118:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 BASE PAIRS
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ATACACTCCC TGATCGAGGA GTCCCAGAAC CAGCAGGAGA AGAATGAA   48

204280_1

(120) INFORMATION FOR SEQ ID NO: 119:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 40 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CAGGCCCGAA GGAATAGAAG AAGAAGGTGG AGAGAGAGAC   40

(121) INFORMATION FOR SEQ ID NO: 120:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 40 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CAGGCCCGAG GGCATCGAGG AGGAGGGCGG CGAGAGAGAC   40

(122) INFORMATION FOR SEQ ID NO: 121:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 50 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TACCACCGCT TGAGAGACTT ACTCTTGATT GTAACGAGGA TTGTGGAACT   50

(123) INFORMATION FOR SEQ ID NO: 122:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 50 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TACCACCGCC TGCGCGACCT GCTCCTGATC GTGACGAGGA TCGTGGAACT   50

(124) INFORMATION FOR SEQ ID NO: 123:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 44 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

GGTGGGAAGC CCTCAAATAT TGGTGGAATC TCCTACAGTA TTGG   44

(125) INFORMATION FOR SEQ ID NO: 124:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 44 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE

```
        (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 124:

GGTGGGAGGC CCTCAAGTAC TGGTGGAACC TCCTCCAGTA TTGG                             44


(126) INFORMATION FOR SEQ ID NO: 125:
        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH:  40 BASE PAIRS
             (B)  TYPE:  NUCLEIC ACID
             (C)  STRANDEDNESS:  SINGLE
             (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 125:

AGTCAGGAAC TAAAGAATAG TGCTGTTAGC TTGCTCAATG                                  40


(127) INFORMATION FOR SEQ ID NO: 126:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH:  40 BASE PAIRS
             (B)  TYPE:  NUCLEIC ACID
             (C)  STRANDEDNESS:  SINGLE
             (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 126:

AGTCAGGAGC TGAAGAACAG CGCCGTGAAC CTGCTCAATG                                  40


(128) INFORMATION FOR SEQ ID NO: 127:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH:  495 BASE PAIRS
             (B)  TYPE:  NUCLEIC ACID
             (C)  STRANDEDNESS:  SINGLE
             (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 127:

GGTACCAGCA CACAAAGGAA TTGGAGGAAA TGAACAAGTA GATAAATTAG TCAGTGCTGG           60

AATCAGGAAA GTACTATTTT TAGATGGAAT AGATAAGGCC CAAGATGAAC ATGAGAAATA           120

TCACAGTAAT TGGAGAGCAA TGGCTAGTGA TTTTAACCTG CCACCTGTAG TAGCAAAAGA           180

AATAGTAGCC AGCTGTGATA AATGTCAGCT AAAAGGAGAA GCCATGCATG GACAAGTAGA           240

CTGTAGTCCA GGAATATGGC AACTAGATTG TACACATTTA GAAGGAAAAG TTATCCTGGT           300

AGCAGTTCAT GTAGCCAGTG GATATATAGA AGCAGAAGTT ATTCCAGCAG AAACAGGGCA           360

GGAAACAGCA TATTTTCTTT TAAAATTAGC AGGAAGATGG CCAGTAAAAA CAATACATAC          420

TGACAATGGC AGCAATTTCA CCGGTGCTAC GGTTAGGGCC GCCTGTTGGT GGGCGGGAAT           480

CAAGCAGGAA TTTGG                                                            495


(129) INFORMATION FOR SEQ ID NO: 128:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH:  7228 BASE PAIRS
             (B)  TYPE:  NUCLEIC ACID
             (C)  STRANDEDNESS:  SINGLE
             (D)  TOPOLOGY:  LINEAR

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 128:
```
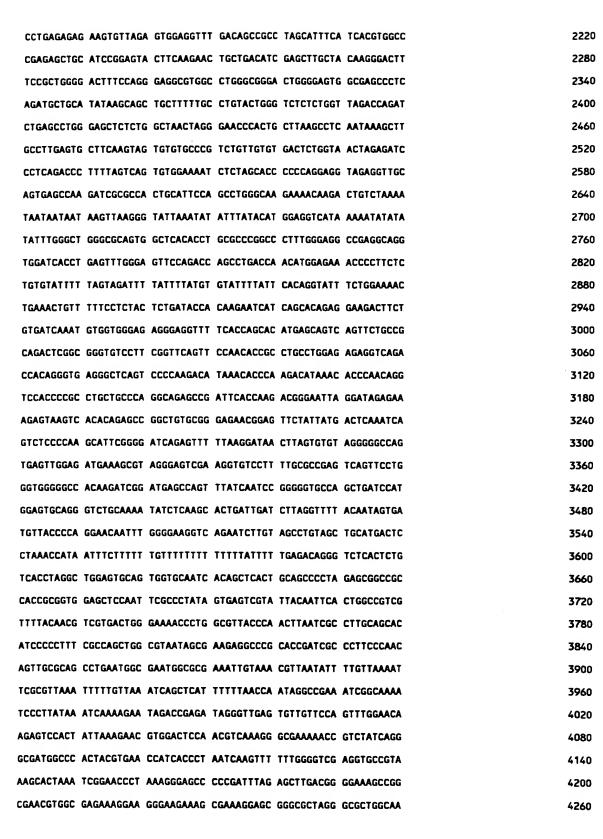
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TGGAAGGGCT AATTTGGTCC CAAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA          60

CACAAGGCTA CTTCCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC         120

TGACCTTTGG ATGGTGCTTC AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA         180

AATAAGGAGA GAAGAACAGC TTGTTACACC CTATGAGCCA GCATGGGATG GAGGACCCGG         240

AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC ATTTCGTCAC ATGGCCCGAG         300

AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG GGACTTTCCG         360

CTGGGGACTT TCCAGGGAGG TGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT         420

GCTACATATA AGCAGCTGCT TTTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA         480

GCCTGGGAGC TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCCT         540

TGAGTGCTCA AAGTAGTGTG TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC         600

AGACCCTTTT AGTCAGTGTG GAAAATCTCT AGCAGTGGCG CCCGAACAGG GACTTGAAAG         660

CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG GCTTGCTGAA GCGCGCGTCG         720

ACAGAGAGAT GGGTGCGAGA GCGTCAGTAT TAAGCGGGGG AGAATTAGAT CGATGGGAAA         780

AAATTCGGTT AAGGCCAGGG GGAAAGAAGA AGTACAAGCT AAAGCACATC GTATGGGCAA         840

GCAGGGAGCT AGAACGATTC GCAGTTAATC CTGGCCTGTT AGAAACATCA GAAGGCTGTA         900

GACAAATACT GGGACAGCTA CAACCATCCC TTCAGACAGG ATCAGAGGAG CTTCGATCAC         960

TATACAACAC AGTAGCAACC CTCTATTGTG TGCACCAGCG GATCGAGATC AAGGACACCA        1020

AGGAAGCTTT AGACAAGATA GAGGAAGAGC AAAACAAGTC CAAGAAGAAG GCCCAGCAGG        1080

CAGCAGCTGA CACAGGACAC AGCAATCAGG TCAGCCAAAA TTACCCTATA GTGCAGAACA        1140

TCCAGGGGCA AATGGTACAT CAGGCCATAT CACCTAGAAC TTTAAATGCA TGGGTAAAAG        1200

TAGTAGAAGA GAAGGCTTTC AGCCCAGAAG TGATACCCAT GTTTTCAGCA TTATCAGAAG        1260

GAGCCACCCC ACAGGACCTG AACACGATGT TGAACACCGT GGGGGGACAT CAAGCAGCCA        1320

TGCAAATGTT AAAAGAGACC ATCAATGAGG AAGCTGCAGA ATGGGATAGA GTGCATCCAG        1380

TGCATGCAGG GCCTATTGCA CCAGGCCAGA TGAGAGAACC AAGGGGAAGT GACATAGCAG        1440

GAACTACTAG TACCCTTCAG GAACAAATAG GATGGATGAC AAATAATCCA CCTATCCCAG        1500

TAGGAGAGAT CTACAAGAGG TGGATAATCC TGGGATTGAA CAAGATCGTG AGGATGTATA        1560

GCCCTACCAG CATTCTGGAC ATAAGACAAG GACCAAAGGA ACCCTTTAGA GACTATGTAG        1620

ACCGGTTCTA TAAAACTCTA AGAGCTGAGC AAGCTTCACA GGAGGTAAAA AATTGGATGA        1680

CAGAAACCTT GTTGGTCCAA AATGCGAACC CAGATTGTAA GACCATCCTG AAGGCTCTCG        1740

GCCCAGCGGC TACACTAGAA GAAATGATGA CAGCATGTCA GGGAGTAGGA GGACCCGGCC        1800

ATAAGGCAAG AGTTTTGTAG GGATCCACTA GTTCTAGACT CGAGGGGGGG CCCGGTACCT        1860

TTAAGACCAA TGACTTACAA GGCAGCTGTA GATCTTAGCC ACTTTTTAAA AGAAAAGGGG        1920

GGACTGGAAG GGCTAATTCA CTCCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC        1980

CACACACAAG GCTACTTCCC TGATTGGCAG AACTACACAC CAGGGCCAGG GGTCAGATAT        2040

CCACTGACCT TTGGATGGTG CTACAAGCTA GTACCAGTTG AGCCAGATAA GGTAGAAGAG        2100

GCCAATAAAG GAGAGAACAC CAGCTTGTTA CACCCTGTGA GCCTGCATGG AATGGATGAC        2160
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CCTGAGAGAG AAGTGTTAGA GTGGAGGTTT GACAGCCGCC TAGCATTTCA TCACGTGGCC          2220

CGAGAGCTGC ATCCGGAGTA CTTCAAGAAC TGCTGACATC GAGCTTGCTA CAAGGGACTT          2280

TCCGCTGGGG ACTTTCCAGG GAGGCGTGGC CTGGGCGGGA CTGGGGAGTG GCGAGCCCTC          2340

AGATGCTGCA TATAAGCAGC TGCTTTTTGC CTGTACTGGG TCTCTCTGGT TAGACCAGAT          2400

CTGAGCCTGG GAGCTCTCTG GCTAACTAGG GAACCCACTG CTTAAGCCTC AATAAAGCTT          2460

GCCTTGAGTG CTTCAAGTAG TGTGTGCCCG TCTGTTGTGT GACTCTGGTA ACTAGAGATC          2520

CCTCAGACCC TTTTAGTCAG TGTGGAAAAT CTCTAGCACC CCCCAGGAGG TAGAGGTTGC          2580

AGTGAGCCAA GATCGCGCCA CTGCATTCCA GCCTGGGCAA GAAAACAAGA CTGTCTAAAA          2640

TAATAATAAT AAGTTAAGGG TATTAAATAT ATTTATACAT GGAGGTCATA AAAATATATA          2700

TATTTGGGCT GGGCGCAGTG GCTCACACCT GCGCCCGGCC CTTTGGGAGG CCGAGGCAGG          2760

TGGATCACCT GAGTTTGGGA GTTCCAGACC AGCCTGACCA ACATGGAGAA ACCCCTTCTC          2820

TGTGTATTTT TAGTAGATTT TATTTTATGT GTATTTTATT CACAGGTATT TCTGGAAAAC          2880

TGAAACTGTT TTTCCTCTAC TCTGATACCA CAAGAATCAT CAGCACAGAG GAAGACTTCT          2940

GTGATCAAAT GTGGTGGGAG AGGGAGGTTT TCACCAGCAC ATGAGCAGTC AGTTCTGCCG          3000

CAGACTCGGC GGGTGTCCTT CGGTTCAGTT CCAACACCGC CTGCCTGGAG AGAGGTCAGA          3060

CCACAGGGTG AGGGCTCAGT CCCCAAGACA TAAACACCCA AGACATAAAC ACCCAACAGG          3120

TCCACCCCGC CTGCTGCCCA GGCAGAGCCG ATTCACCAAG ACGGGAATTA GGATAGAGAA          3180

AGAGTAAGTC ACACAGAGCC GGCTGTGCGG GAGAACGGAG TTCTATTATG ACTCAAATCA          3240

GTCTCCCCAA GCATTCGGGG ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG          3300

TGAGTTGGAG ATGAAAGCGT AGGGAGTCGA AGGTGTCCTT TTGCGCCGAG TCAGTTCCTG          3360

GGTGGGGGCC ACAAGATCGG ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT          3420

GGAGTGCAGG GTCTGCAAAA TATCTCAAGC ACTGATTGAT CTTAGGTTTT ACAATAGTGA          3480

TGTTACCCCA GGAACAATTT GGGGAAGGTC AGAATCTTGT AGCCTGTAGC TGCATGACTC          3540

CTAAACCATA ATTTCTTTTT TGTTTTTTTT TTTTTATTTT TGAGACAGGG TCTCACTCTG          3600

TCACCTAGGC TGGAGTGCAG TGGTGCAATC ACAGCTCACT GCAGCCCCTA GAGCGGCCGC          3660

CACCGCGGTG GAGCTCCAAT TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG          3720

TTTTACAACG TCGTGACTGG GAAAACCCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC          3780

ATCCCCCTTT CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC          3840

AGTTGCGCAG CCTGAATGGC GAATGGCGCG AAATTGTAAA CGTTAATATT TTGTTAAAAT          3900

TCGCGTTAAA TTTTTGTTAA ATCAGCTCAT TTTTTAACCA ATAGGCCGAA ATCGGCAAAA          3960

TCCCTTATAA ATCAAAAGAA TAGACCGAGA TAGGGTTGAG TGTTGTTCCA GTTTGGAACA          4020

AGAGTCCACT ATTAAAGAAC GTGGACTCCA ACGTCAAAGG GCGAAAAACC GTCTATCAGG          4080

GCGATGGCCC ACTACGTGAA CCATCACCCT AATCAAGTTT TTTGGGGTCG AGGTGCCGTA          4140

AAGCACTAAA TCGGAACCCT AAAGGGAGCC CCCGATTTAG AGCTTGACGG GGAAAGCCGG          4200

CGAACGTGGC GAGAAAGGAA GGGAAGAAAG CGAAAGGAGC GGGCGCTAGG GCGCTGGCAA          4260
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GTGTAGCGGT CACGCTGCGC GTAACCACCA CACCCGCCGC GCTTAATGCG CCGCTACAGG          4320

GCGCGTCCCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCCTATTT GTTTATTTTT          4380

CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCAATA          4440

ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT          4500

TGCGGCATTT TGCCTTCCTG TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC          4560

TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT          4620

CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG AGCACTTTTA AAGTTCTGCT          4680

ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG CAACTCGGTC GCCGCATACA          4740

CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG          4800

CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA          4860

CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG          4920

GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA          4980

CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAACG TTGCGCAAAC TATTAACTGG          5040

CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT          5100

TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG          5160

AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC          5220

CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA          5280

GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC          5340

ATATATACTT TAGATTGATT TAAAACTTCA TTTTTAATTT AAAAGGATCT AGGTGAAGAT          5400

CCTTTTTGAT AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC          5460

AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTTTCTGC GCGTAATCTG          5520

CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT TGTTTGCCGG ATCAAGAGCT          5580

ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCCT          5640

TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT          5700

CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG          5760

GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA CGGGGGGTTC          5820

GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA          5880

GCTATGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG          5940

CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA          6000

TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG          6060

GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC TGGCCTTTTG          6120

CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG ATAACCGTAT          6180

TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC          6240

AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC          6300

GATTCATTAA TGCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA          6360

CGCAATTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC          6420
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GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA          6480

CCATGATTAC GCCAAGCTCG GAATTAACCC TCACTAAAGG GAACAAAAGC TGCTGCAGGG          6540

TCCCTAACTG CCAAGCCCCA CAGTGTGCCC TGAGGCTGCC CCTTCCTTCT AGCGGCTGCC          6600

CCCACTCGGC TTTGCTTTCC CTAGTTTCAG TTACTTGCGT TCAGCCAAGG TCTGAAACTA          6660

GGTGCGCACA GAGCGGTAAG ACTGCGAGAG AAAGAGACCA GCTTTACAGG GGGTTTATCA          6720

CAGTGCACCC TGACAGTCGT CAGCCTCACA GGGGGTTTAT CACATTGCAC CCTGACAGTC          6780

GTCAGCCTCA CAGGGGGTTT ATCACAGTGC ACCCTTACAA TCATTCCATT TGATTCACAA          6840

TTTTTTTAGT CTCTACTGTG CCTAACTTGT AAGTTAAATT TGATCAGAGG TGTGTTCCCA          6900

GAGGGGAAAA CAGTATATAC AGGGTTCAGT ACTATCGCAT TTCAGGCCTC CACCTGGGTC          6960

TTGGAATGTG TCCCCCGAGG GGTGATGACT ACCTCAGTTG GATCTCCACA GGTCACAGTG          7020

ACACAAGATA ACCAAGACAC CTCCCAAGGC TACCACAATG GGCCGCCCTC CACGTGCACA          7080

TGGCCGGAGG AACTGCCATG TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCTTGGTG          7140

TGGAGGGAGG GACCAGCGCA GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGAAAG          7200

CCCCAGTTCT ACTTACACCA GGAAAGGC                                            7228
```

(130) INFORMATION FOR SEQ ID NO: 129

      (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 7228 BASE PAIRS
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

      (ix)   SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```
TGGAAGGGCT AATTTGGTCC CAAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA          60

CACAAGGCTA CTTCCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC          120

TGACCTTTGG ATGGTGCTTC AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA          180

AATAAGGAGA GAAGAACAGC TTGTTACACC CTATGAGCCA GCATGGGATG GAGGACCCGG          240

AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC ATTTCGTCAC ATGGCCCGAG          300

AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG GGACTTTCCG          360

CTGGGGACTT TCCAGGGAGG TGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT          420

GCTACATATA AGCAGCTGCT TTTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA          480

GCCTGGGAGC TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCCT          540

TGAGTGCTCA AAGTAGTGTG TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC          600

AGACCCTTTT AGTCAGTGTG GAAAATCTCT AGCAGTGGCG CCCGAACAGG GACTTGAAAG          660

CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG GCTTGCTGAA GCGCGCGTCG          720
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ACAGAGAG ATG GGT GCG AGA GCG TCA GTA TTA AGC GGG GGA GAA TTA GAT          770
         Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp
          1               5                   10

CGA TGG GAA AAA ATT CGG TTA AGG CCA GGG GGA AAG AAG AAG TAC AAG          818
Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys
15               20                  25                  30
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CTA AAG CAC ATC GTA TGG GCA AGC AGG GAG CTA GAA CGA TTC GCA GTT        866
Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val
        35              40                  45

AAT CCT GGC CTG TTA GAA ACA TCA GAA GGC TGT AGA CAA ATA CTG GGA        914
Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly
        50              55                  60

CAG CTA CAA CCA TCC CTT CAG ACA GGA TCA GAG GAG CTT CGA TCA CTA        962
Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu
        65              70              75

TAC AAC ACA GTA GCA ACC CTC TAT TGT GTG CAC CAG CGG ATC GAG ATC       1010
Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile
        80              85              90

AAG GAC ACC AAG GAA GCT TTA GAC AAG ATA GAG GAA GAG CAA AAC AAG       1058
Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys
95              100             105             110

TCC AAG AAG AAG GCC CAG CAG GCA GCA GCT GAC ACA GGA CAC AGC AAT       1106
Ser Lys Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn
111             115             120             125

CAG GTC AGC CAA AAT TAC CCT ATA GTG CAG AAC ATC CAG GGG CAA ATG       1154
Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met
        130             135             140

GTA CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA AAA GTA       1202
Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
        145             150             155

GTA GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT TCA GCA       1250
Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
        160             165             170

TTA TCA GAA GGA GCC ACC CCA CAG GAC CTG AAC ACG ATG TTG AAC ACC       1298
Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
175             180             185             190

GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACC ATC AAT       1346
Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn
        195             200             205

GAG GAA GCT GCA GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA GGG CCT       1394
Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro
        210             215             220

ATT GCA CCA GGC CAG ATG AGA GAA CCA AGG GGA AGT GAC ATA GCA GGA       1442
Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly
        225             230             235

ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG ACA AAT AAT CCA       1490
Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro
        240             245             250

CCT ATC CCA GTA GGA GAG ATC TAC AAG AGG TGG ATA ATC CTG GGA TTG       1538
Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu
255             260             265             270

AAC AAG ATC GTG AGG ATG TAT AGC CCT ACC AGC ATT CTG GAC ATA AGA       1586
Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg
        275             280             285

CAA GGA CCA AAG GAA CCC TTT AGA GAC TAT GTA GAC CGG TTC TAT AAA       1634
Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
        290             295             300

ACT CTA AGA GCT GAG CAA GCT TCA CAG GAG GTA AAA AAT TGG ATG ACA       1682
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        Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr
                305             310             315
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        GAA ACC TTG TTG GTC CAA AAT GCG AAC CCA GAT TGT AAG ACC ATC CTG         1730
        Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu
            320             325             330
```

```
        AAG GCT CTC GGC CCA GCG GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT         1778
        Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys
        335             340             345             350
```

```
        CAG GGA GTA GGA GGA CCC GGC CAT AAG GCA AGA GTT TTG TAG             1820
        Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu
                    355             360
```

```
        GGATCCACTA GTTCTAGACT CGAGGGGGGG CCCGGTACCT TTAAGACCAA TGACTTACAA         1880

        GGCAGCTGTA GATCTTAGCC ACTTTTTAAA AGAAAAGGGG GGACTGGAAG GGCTAATTCA         1940

        CTCCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC CACACACAAG GCTACTTCCC         2000

        TGATTGGCAG AACTACACAC CAGGGCCAGG GGTCAGATAT CCACTGACCT TTGGATGGTG         2060

        CTACAAGCTA GTACCAGTTG AGCCAGATAA GGTAGAAGAG GCCAATAAAG GAGAGAACAC         2120

        CAGCTTGTTA CACCCTGTGA GCCTGCATGG AATGGATGAC CCTGAGAGAG AAGTGTTAGA         2180

        GTGGAGGTTT GACAGCCGCC TAGCATTTCA TCACGTGGCC CGAGAGCTGC ATCCGGAGTA         2240

        CTTCAAGAAC TGCTGACATC GAGCTTGCTA CAAGGGACTT TCCGCTGGGG ACTTTCCAGG         2300

        GAGGCGTGGC CTGGGCGGGA CTGGGGAGTG GCGAGCCCTC AGATGCTGCA TATAAGCAGC         2360

        TGCTTTTTGC CTGTACTGGG TCTCTCTGGT TAGACCAGAT CTGAGCCTGG GAGCTCTCTG         2420

        GCTAACTAGG GAACCCACTG CTTAAGCCTC AATAAAGCTT GCCTTGAGTG CTTCAAGTAG         2480

        TGTGTGCCCG TCTGTTGTGT GACTCTGGTA ACTAGAGATC CCTCAGACCC TTTTAGTCAG         2540

        TGTGGAAAAT CTCTAGCACC CCCAGGAGG TAGAGGTTGC AGTGAGCCAA GATCGCGCCA         2600

        CTGCATTCCA GCCTGGGCAA GAAAACAAGA CTGTCTAAAA TAATAATAAT AAGTTAAGGG         2660

        TATTAAATAT ATTTATACAT GGAGGTCATA AAAATATATA TATTTGGGCT GGGCGCAGTG         2720

        GCTCACACCT GCGCCCGGCC CTTTGGGAGG CCGAGGCAGG TGGATCACCT GAGTTTGGGA         2780

        GTTCCAGACC AGCCTGACCA ACATGGAGAA ACCCCTTCTC TGTGTATTTT TAGTAGATTT         2840

        TATTTTATGT GTATTTTATT CACAGGTATT TCTGGAAAAC TGAAACTGTT TTTCCTCTAC         2900

        TCTGATACCA CAAGAATCAT CAGCACAGA GAAGACTTCT GTGATCAAAT GTGGTGGGAG         2960

        AGGGAGGTTT TCACCAGCAC ATGAGCAGTC AGTTCTGCCG CAGACTCGGC GGGTGTCCTT         3020

        CGGTTCAGTT CCAACACCGC CTGCCTGGAG AGAGGTCAGA CCACAGGGTG AGGGCTCAGT         3080

        CCCCAAGACA TAAACACCCA AGACATAAAC ACCCAACAGG TCCACCCCGC CTGCTGCCCA         3140

        GGCAGAGCCG ATTCACCAAG ACGGGAATTA GGATAGAGAA AGAGTAAGTC ACACAGAGCC         3200

        GGCTGTGCGG GAGAACGGAG TTCTATTATG ACTCAAATCA GTCTCCCCAA GCATTCGGGG         3260

        ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG TGAGTTGGAG ATGAAAGCGT         3320

        AGGGAGTCGA AGGTGTCCTT TTGCGCCGAG TCAGTTCCTG GGTGGGGGCC ACAAGATCGG         3380

        ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT GGAGTGCAGG GTCTGCAAAA         3440

        TATCTCAAGC ACTGATTGAT CTTAGGTTTT ACAATAGTGA TGTTACCCCA GGAACAATTT         3500
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GGGGAAGGTC AGAATCTTGT AGCCTGTAGC TGCATGACTC CTAAACCATA ATTTCTTTTT          3560

TGTTTTTTTT TTTTTATTTT TGAGACAGGG TCTCACTCTG TCACCTAGGC TGGAGTGCAG          3620

TGGTGCAATC ACAGCTCACT GCAGCCCCTA GAGCGGCCGC CACCGCGGTG GAGCTCCAAT          3680

TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG TTTTACAACG TCGTGACTGG          3740

GAAAACCCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT CGCCAGCTGG          3800

CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC          3860

GAATGGCGCG AAATTGTAAA CGTTAATATT TTGTTAAAAT TCGCGTTAAA TTTTTGTTAA          3920

ATCAGCTCAT TTTTTAACCA ATAGGCCGAA ATCGGCAAAA TCCCTTATAA ATCAAAAGAA          3980

TAGACCGAGA TAGGGTTGAG TGTTGTTCCA GTTTGGAACA AGAGTCCACT ATTAAAGAAC          4040

GTGGACTCCA ACGTCAAAGG GCGAAAAACC GTCTATCAGG GCGATGGCCC ACTACGTGAA          4100

CCATCACCCT AATCAAGTTT TTTGGGGTCG AGGTGCCGTA AAGCACTAAA TCGGAACCCT          4160

AAAGGGAGCC CCCGATTTAG AGCTTGACGG GGAAAGCCGG CGAACGTGGC GAGAAAGGAA          4220

GGGAAGAAAG CGAAAGGAGC GGGCGCTAGG GCGCTGGCAA GTGTAGCGGT CACGCTGCGC          4280

GTAACCACCA CACCCGCCGC GCTTAATGCG CCGCTACAGG GCGCGTCCCA GGTGGCACTT          4340

TTCGGGGAAA TGTGCGCGGA ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT          4400

ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA          4460

TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG          4520

TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC          4580

GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG          4640

AAGAACGTTT TCCAATGATG AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC          4700

GTATTGACGC CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG          4760

TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT          4820

GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG          4880

GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG          4940

ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC          5000

CTGTAGCAAT GGCAACAACG TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT          5060

CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT          5120

CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC          5180

GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA          5240

CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT          5300

CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT          5360

TAAAACTTCA TTTTTAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT AATCTCATGA          5420

CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA          5480

AAGGATCTTC TTGAGATCCT TTTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC          5540

CACCGCTACC AGCGGTGGTT TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG          5600

TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG          5660
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GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC    5720

CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT    5780

TACCGGATAA GGCGCAGCGG TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG    5840

AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC    5900

TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC    5960

GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC    6020

ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA    6080

ACGCCAGCAA CGCGGCCTTT TTACGGTTCC TGGCCTTTTG CTGGCCTTTT GCTCACATGT    6140

TCTTTCCTGC GTTATCCCCT GATTCTGTGG ATAACCGTAT TACCGCCTTT GAGTGAGCTG    6200

ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG    6260

AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA TGCAGCTGGC    6320

ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTAGC    6380

TCACTCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA    6440

TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTCG    6500

GAATTAACCC TCACTAAAGG GAACAAAAGC TGCTGCAGGG TCCCTAACTG CCAAGCCCCA    6560

CAGTGTGCCC TGAGGCTGCC CCTTCCTTCT AGCGGCTGCC CCCACTCGGC TTTGCTTTCC    6620

CTAGTTTCAG TTACTTGCGT TCAGCCAAGG TCTGAAACTA GGTGCGCACA GAGCGGTAAG    6680

ACTGCGAGAG AAAGAGACCA GCTTTACAGG GGGTTTATCA CAGTGCACCC TGACAGTCGT    6740

CAGCCTCACA GGGGGTTTAT CACATTGCAC CCTGACAGTC GTCAGCCTCA CAGGGGGTTT    6800

ATCACAGTGC ACCCTTACAA TCATTCCATT TGATTCACAA TTTTTTTAGT CTCTACTGTG    6860

CCTAACTTGT AAGTTAAATT TGATCAGAGG TGTGTTCCCA GAGGGGAAAA CAGTATATAC    6920

AGGGTTCAGT ACTATCGCAT TTCAGGCCTC CACCTGGGTC TTGGAATGTG TCCCCCGAGG    6980

GGTGATGACT ACCTCAGTTG GATCTCCACA GGTCACAGTG ACACAAGATA ACCAAGACAC    7040

CTCCCAAGGC TACCACAATG GGCCGCCCTC CACGTGCACA TGGCCGGAGG AACTGCCATG    7100

TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCTTGGTG TGGAGGGAGG GACCAGCGCA    7160

GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGAAAG CCCCAGTTCT ACTTACACCA    7220

GGAAAGGC                                                            7228
```

(131) INFORMATION FOR SEQ ID NO: 130:

      (i)   SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 363 AMINO ACIDS
           (B) TYPE: AMINO ACID
           (C) TOPOLOGY: LINEAR

      (ii)   MOLECULAR TYPE: PROTEIN

      (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 130

```
Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1               5                   10                  15
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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
             20   25   30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
         35   40   45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
     50   55   60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65   70   75   80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
         85   90   95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
         100   105   110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
         115   120   125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
         130   135   140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145   150   155   160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
         165   170   175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
         180   185   190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
         195   200   205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
         210   215   220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225   230   235   240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
         245   250   255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
         260   265   270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
         275   280   285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
         290   295   300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305   310   315   320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
         325   330   335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
         340   345   350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu
         355   360